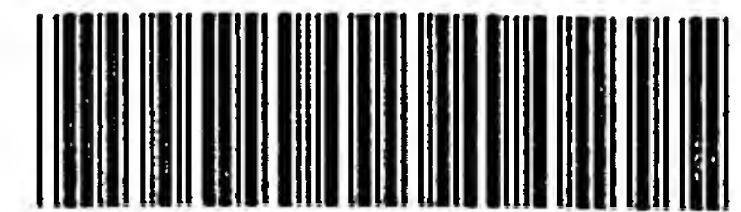# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: /0/59/,628

Source: LFWP

Date Processed by STIC: 9/13/06

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RAW SEQUENCE LISTING   DATE: 09/13/2006
PATENT APPLICATION: US/10/591,628   TIME: 11:11:47

Input Set : **A:\A0852.70000US01 seq.txt**
Output Set: **N:\CRF4\09132006\J591628.raw**

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  3 <110> APPLICANT: Adra, Chaker
  5 <120> TITLE OF INVENTION: GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND
USES
  6         THEREOF
  8 <130> FILE REFERENCE: A0852.70000WO00
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,628
 11 <141> CURRENT FILING DATE: 2006-09-05
 13 <150> PRIOR APPLICATION NUMBER: PCT/US2005/007519
 14 <151> PRIOR FILING DATE: 2005-03-03
 16 <150> PRIOR APPLICATION NUMBER: 60/549,865
 17 <151> PRIOR FILING DATE: 2004-03-03
 19 <160> NUMBER OF SEQ ID NOS: 31
 21 <170> SOFTWARE: PatentIn version 3.3
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 24 <211> LENGTH: 557
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
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 31 ctgtagtgtc aagttctttc aaacttaaaa ttttaacccc agaggatttt cgctgaataa      120
 33 atgagaattg gctctatttc ttctacttct ggatagcccg agtaaaaata ctaataattt      180
 35 ctagatttta gtggggaact acaattatta ggacccatgg atattgctgc agttcaaata      240
 37 caatacagta attacaaaat atagaccatc tctttacaaa tacaaattat agtatattac      300
 39 aagtcatgta cagtaaatct ataattttaa acaaactagt gtatctaagt ttacctggtt      360
 41 gcgagtgcat tattattcca gtttacagtt gcccttagcg tgacagtcag aaaccgacca      420
 43 tcggagtgat attctcttat gtaaactggc gtcacatcac agaaaacctt atttatgagg      480
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 47 tcagaacagc taaacag                                                     557
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 52 <212> TYPE: DNA
 53 <213> ORGANISM: Homo sapiens
 55 <220> FEATURE:
 56 <221> NAME/KEY: CDS
 57 <222> LOCATION: (71)..(1198)
 59 <400> SEQUENCE: 2
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 62 gagcctggca atg gat gcc att cac atc ggc atg tcc agc acc ccc ctg        109
 63             Met Asp Ala Ile His Ile Gly Met Ser Ser Thr Pro Leu
 64              1               5                  10
 66 gtg aag cac act gct ggg gct ggg ctc aag gcc aac aga ccc cgc gtc       157
 67 Val Lys His Thr Ala Gly Ala Gly Leu Lys Ala Asn Arg Pro Arg Val
 68    15                  20                  25
 70 atg tcc aag agt ggg cac agc aac gtg aga att gac aaa gtg gat ggc       205
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71  Met Ser Lys Ser Gly His Ser Asn Val Arg Ile Asp Lys Val Asp Gly
72  30                  35                  40                  45
74  ata tac cta ctc tac ctg caa gac ctg tgg acc aca gtt atc gac atg     253
75  Ile Tyr Leu Leu Tyr Leu Gln Asp Leu Trp Thr Thr Val Ile Asp Met
76                  50                  55                  60
78  aag tgg aga tac aaa ctc acc ctg ttc gct gcc act ttt gtg atg acc     301
79  Lys Trp Arg Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr
80              65                  70                  75
82  tgg ttc ctt ttt gga gtc atc tac tat gcc atc gcg ttt att cat ggg     349
83  Trp Phe Leu Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly
84              80                  85                  90
86  gac tta gaa ccc gat gag ccc att tca aat cat acc ccc tgc atc atg     397
87  Asp Leu Glu Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met
88      95                  100                 105
90  aaa gtg gac tct ctc act ggg gcg ttt ctc ttt tcc ctg gaa tcc cag     445
91  Lys Val Asp Ser Leu Thr Gly Ala Phe Leu Phe Ser Leu Glu Ser Gln
92  110                 115                 120                 125
94  aca acc att ggc tat gga gtc cgt tcc atc aca gag gaa tgt cct cat     493
95  Thr Thr Ile Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His
96                  130                 135                 140
98  gcc atc ttc ctg ttg gtt gct cag ttg gtc atc acg acc ttg att gag     541
99  Ala Ile Phe Leu Leu Val Ala Gln Leu Val Ile Thr Thr Leu Ile Glu
100                 145                 150                 155
102 atc ttc atc acc gga acc ttc ctg gcc aaa atc gcc aga ccc aaa aag     589
103 Ile Phe Ile Thr Gly Thr Phe Leu Ala Lys Ile Ala Arg Pro Lys Lys
104             160                 165                 170
106 cgg gct gag acc atc aag ttc agc cac tgt gca gtc atc acc aag cag     637
107 Arg Ala Glu Thr Ile Lys Phe Ser His Cys Ala Val Ile Thr Lys Gln
108     175                 180                 185
110 aat ggg aag ctg tgc ttg gtg att cag gta gcc aat atg agg aag agc     685
111 Asn Gly Lys Leu Cys Leu Val Ile Gln Val Ala Asn Met Arg Lys Ser
112 190                 195                 200                 205
114 ctc ttg att cag tgc cag ctc tct ggc aag ctc ctg cag acc cac gtc     733
115 Leu Leu Ile Gln Cys Gln Leu Ser Gly Lys Leu Leu Gln Thr His Val
116                 210                 215                 220
118 acc aag gag ggg gag cgg att ctc ctc aac caa gcc act gtc aaa ttc     781
119 Thr Lys Glu Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe
120                 225                 230                 235
122 cac gtg gac tcc tcc tct gag agc ccc ttc ctc att ctg ccc atg aca     829
123 His Val Asp Ser Ser Ser Glu Ser Pro Phe Leu Ile Leu Pro Met Thr
124             240                 245                 250
125 ttc tac cat gtg ctg gat gag acg agc ccc ctg aga gac ctc aca ccc     877
126 Phe Tyr His Val Leu Asp Glu Thr Ser Pro Leu Arg Asp Leu Thr Pro
127     255                 260                 265
129 caa aac cta aag gag aag gag ttt gag ctt gtg gtc ctc ctc aat gcc     925
130 Gln Asn Leu Lys Glu Lys Glu Phe Glu Leu Val Val Leu Leu Asn Ala
131 270                 275                 280                 285
133 act gtg gaa tcc acc agc gct gtc tgc cag agc cga aca tct tat atc     973
134 Thr Val Glu Ser Thr Ser Ala Val Cys Gln Ser Arg Thr Ser Tyr Ile
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RAW SEQUENCE LISTING   DATE: 09/13/2006
PATENT APPLICATION: US/10/591,628   TIME: 11:11:47

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Output Set: N:\CRF4\09132006\J591628.raw

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137 cca gag gaa atc tac tgg ggt ttt gag ttt gtg cct gtg gta tct ctc        1021
138 Pro Glu Glu Ile Tyr Trp Gly Phe Glu Phe Val Pro Val Val Ser Leu
139                 305              310              315
141 tcc aaa aat gga aaa tat gtg gct gat ttc agt cag ttt gaa cag att        1069
142 Ser Lys Asn Gly Lys Tyr Val Ala Asp Phe Ser Gln Phe Glu Gln Ile
143                 320              325              330
145 cgg aaa agc cca gat tgc aca ttt tac tgt gca gat tct gag aaa cag        1117
146 Arg Lys Ser Pro Asp Cys Thr Phe Tyr Cys Ala Asp Ser Glu Lys Gln
147       335              340              345
149 caa ctc gag gag aag tac agg cag gag gat cag agg gaa aga gaa ctg        1165
150 Gln Leu Glu Glu Lys Tyr Arg Gln Glu Asp Gln Arg Glu Arg Glu Leu
151 350              355              360              365
153 agg aca ctt tta tta caa cag agc aat gtc tga tcacaggggc gccatccagg     1218
154 Arg Thr Leu Leu Leu Gln Gln Ser Asn Val
155                 370              375
157 tttaaccctg caagctgttt ccacatcaga actcccttca aacacaaaga ttgctgtgaa     1278
159 aacgaaaatg tgtagacgca ctctcaaaaa ctgcacggac atacaaaatc aatcttttcc     1338
161 tttgatcttg tggctaaacc agcatttctg tgtttgagag atttcctgtt aggtgcttcg     1398
163 tctgaaagtg aactctcata attcaaattg tataaataa agctacattt ctaagagctt      1458
165 ggtgtagggc aattggaata atgtcctgtt agataaacag acatttagca atgctgacat     1518
167 taaaaggaaa tgtatttcta tacaagatta ttagctgtaa tacaagatat ttatttaacc    1578
169 aatgacctta tggctgagag ttgaattgtg gttca                               1613
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 375
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 3
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184             20               25               30
187 Ser Gly His Ser Asn Val Arg Ile Asp Lys Val Asp Gly Ile Tyr Leu
188         35               40               45
191 Leu Tyr Leu Gln Asp Leu Trp Thr Thr Val Ile Asp Met Lys Trp Arg
192     50               55               60
195 Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr Trp Phe Leu
196 65               70               75               80
199 Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly Asp Leu Glu
200             85               90               95
203 Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met Lys Val Asp
204             100              105              110
207 Ser Leu Thr Gly Ala Phe Leu Phe Ser Leu Glu Ser Gln Thr Thr Ile
208         115              120              125
211 Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His Ala Ile Phe
212     130              135              140
215 Leu Leu Val Ala Gln Leu Val Ile Thr Thr Leu Ile Glu Ile Phe Ile
216 145              150              155              160
219 Thr Gly Thr Phe Leu Ala Lys Ile Ala Arg Pro Lys Lys Arg Ala Glu
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220                   165            170              175
223 Thr Ile Lys Phe Ser His Cys Ala Val Ile Thr Lys Gln Asn Gly Lys
224               180            185            190
227 Leu Cys Leu Val Ile Gln Val Ala Asn Met Arg Lys Ser Leu Leu Ile
228           195            200            205
231 Gln Cys Gln Leu Ser Gly Lys Leu Leu Gln Thr His Val Thr Lys Glu
232       210            215            220
235 Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe His Val Asp
236 225            230            235              240
239 Ser Ser Ser Glu Ser Pro Phe Leu Ile Leu Pro Met Thr Phe Tyr His
240           245            250            255
243 Val Leu Asp Glu Thr Ser Pro Leu Arg Asp Leu Thr Pro Gln Asn Leu
244           260            265            270
247 Lys Glu Lys Glu Phe Glu Leu Val Val Leu Leu Asn Ala Thr Val Glu
248       275            280            285
249 Ser Thr Ser Ala Val Cys Gln Ser Arg Thr Ser Tyr Ile Pro Glu Glu
250       290            295            300
253 Ile Tyr Trp Gly Phe Glu Phe Val Pro Val Val Ser Leu Ser Lys Asn
254 305            310            315            320
257 Gly Lys Tyr Val Ala Asp Phe Ser Gln Phe Glu Gln Ile Arg Lys Ser
258           325            330            335
261 Pro Asp Cys Thr Phe Tyr Cys Ala Asp Ser Glu Lys Gln Gln Leu Glu
262       340            345            350
265 Glu Lys Tyr Arg Gln Glu Asp Gln Arg Glu Arg Glu Leu Arg Thr Leu
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273 <210> SEQ ID NO: 4
274 <211> LENGTH: 5397
275 <212> TYPE: DNA
276 <213> ORGANISM: Homo sapiens
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (384)..(1667)
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287 accccccact tccactccat gtccccatgc tcctgcgcca gcaacaggac atgttctctg    180
289 gatgtcagct gagtcattaa agtaactctg catgtcagta gacagacctt ggtagaacca    240
291 caaggctccc agagacaccc atctctcctc attttttttgg tgtgtgtgtc ttcaccgaac    300
293 attcaaaact gtttctccaa agcgttttgc aaaaactcag actgttttcc aaagcagaag    360
295 cactggagtc cccagcagaa gcg atg ggc agt gtg cga acc aac cgc tac agc    413
296                         Met Gly Ser Val Arg Thr Asn Arg Tyr Ser
297                          1            5                  10
299 atc gtc tct tca gaa gaa gac ggt atg aag ttg gcc acc atg gca gtt    461
300 Ile Val Ser Ser Glu Glu Asp Gly Met Lys Leu Ala Thr Met Ala Val
301               15            20            25
303 gca aat ggc ttt ggg aac ggg aag agt aaa gtc cac acc cga caa cag    509
304 Ala Asn Gly Phe Gly Asn Gly Lys Ser Lys Val His Thr Arg Gln Gln
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PATENT APPLICATION: **US/10/591,628**   TIME: 11:11:47

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Output Set: **N:\CRF4\09132006\J591628.raw**

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307 tgc agg agc cgc ttt gtg aag aaa gat ggc cac tgt aat gtt cag ttc    557
308 Cys Arg Ser Arg Phe Val Lys Lys Asp Gly His Cys Asn Val Gln Phe
309         45              50              55
311 atc aat gtg ggt gag aag ggg caa cgg tac ctc gca gac atc ttc acc    605
312 Ile Asn Val Gly Glu Lys Gly Gln Arg Tyr Leu Ala Asp Ile Phe Thr
313     60              65              70
315 acg tgt gtg gac att cgc tgg cgg tgg atg ctg gtt atc ttc tgc ctg    653
316 Thr Cys Val Asp Ile Arg Trp Arg Trp Met Leu Val Ile Phe Cys Leu
317 75              80              85              90
319 gct ttc gtc ctg tca tgg ctg ttt ttt ggc tgt gtg ttt tgg ttg ata    701
320 Ala Phe Val Leu Ser Trp Leu Phe Phe Gly Cys Val Phe Trp Leu Ile
321             95              100             105
323 gct ctg ctc cat ggg gac ctg gat gca tcc aaa gag ggc aaa gct tgt    749
324 Ala Leu Leu His Gly Asp Leu Asp Ala Ser Lys Glu Gly Lys Ala Cys
325             110             115             120
327 gtg tcc gag gtc aac agc ttc acg gct gcc ttc ctc ttc tcc att gag    797
328 Val Ser Glu Val Asn Ser Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu
329         125             130             135
331 acc cag aca acc ata ggc tat ggt ttc aga tgt gtc acg gat gaa tgc    845
332 Thr Gln Thr Thr Ile Gly Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys
333     140             145             150
335 cca att gct gtt ttc atg gtg gtg ttc cag tca atc gtg ggc tgc atc    893
336 Pro Ile Ala Val Phe Met Val Val Phe Gln Ser Ile Val Gly Cys Ile
337 155             160             165             170
339 atc gat gct ttc atc att ggc gca gtc atg gcc aag atg gca aag cca    941
340 Ile Asp Ala Phe Ile Ile Gly Ala Val Met Ala Lys Met Ala Lys Pro
341             175             180             185
343 aag aag aga aac gag act ctt gtc ttc agt cac aat gcc gtg att gcc    989
344 Lys Lys Arg Asn Glu Thr Leu Val Phe Ser His Asn Ala Val Ile Ala
345         190             195             200
347 atg aga gac ggc aag ctg tgt ttg atg tgg cga gtg ggc aat ctt cgg   1037
348 Met Arg Asp Gly Lys Leu Cys Leu Met Trp Arg Val Gly Asn Leu Arg
349         205             210             215
351 aaa agc cac ttg gtg gaa gct cat gtt cga gca cag ctc ctc aaa tcc   1085
352 Lys Ser His Leu Val Glu Ala His Val Arg Ala Gln Leu Leu Lys Ser
353     220             225             230
355 aga att act tct gaa ggg gag tat atc cct ctg gat caa ata gac atc   1133
356 Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile
357 235             240             245             250
359 aat gtt ggg ttt gac agt gga atc gat cgt ata ttt ctg gtg tcc cca   1181
360 Asn Val Gly Phe Asp Ser Gly Ile Asp Arg Ile Phe Leu Val Ser Pro
361             255             260             265
363 atc act ata gtc cat gaa ata gat gaa gac agt cct tta tat gat ttg   1229
364 Ile Thr Ile Val His Glu Ile Asp Glu Asp Ser Pro Leu Tyr Asp Leu
365             270             275             280
367 agt aaa cag gac att gac aac gca gac ttt gaa atc gtg gtc ata ctg   1277
368 Ser Lys Gln Asp Ile Asp Asn Ala Asp Phe Glu Ile Val Val Ile Leu
369     285             290             295
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VERIFICATION SUMMARY   DATE: 09/13/2006
PATENT APPLICATION: **US/10/591,628**   TIME: 11:11:48

Input Set : **A:\A0852.70000US01 seq.txt**
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number